

QY 1202 VFYKKDNETI-PCYRERISMHODTGVACLLIQPAKKSDAGWYLSAKNEAGIVSCTAR 1260
 Db 1314 DIVVLKNSDIIVPHKYPRI-ECTKGAAALNIESTARQDAANYTATNKKAG--RDTTR 1370
 QY 1361 LDYVACWHQIOPP 1274
 Db 1371 CKVNEVEHAPEP 1384

RESULT 3
 138344 cardiac muscle [validated] - human
 A:Alternate names: connectin
 N:Contents: serine/threonine-specific protein kinase (EC 2.7.1.1-)
 C:Species: Homo sapiens (man)
 C:Date: 12-Aug-1996 #sequence revision 12-Aug-1996 #text change 15-Sep-2000
 C:Accession: I38344; I38345; S20898; S20897; S20899; S63665; S37393
 R:Label: S.; Kolmerer, B.
 Science 270, 293-296, 1995
 A:Title: Titins: giant proteins in charge of muscle ultrastructure and elasticity.
 A:Reference number: A37430; MUID:96026330; PMID:7569978
 A:Accession: I38344
 A:Status: nucleic acid sequence not shown; translation not shown; translated from GB/EMBL
 A:Molecule type: mRNA
 A:Residues: 1-25926 <LAB1>
 A:Cross-references: EMBL:X90568; NID:gl017424; PID:g1017425
 R:Musco G.; Tziatios, C.; Schuck, P.; Pastore, A.
 Biogenetstry 34, 553-561, 1995
 A:Title: Dissecting titin into its structural motifs: Identification of an alpha-helix in
 A:Reference number: I38345; MUID:95119041; PMID:7819249
 A:Accession: I38345
 A:Status: nucleic acid sequence not shown
 A:Molecule type: mRNA
 A:Residues: 1977-2014 <MUS>
 A:Cross-references: EMBL:X83270; NID:g602579; PIDN:CAA58243.1; PID:g602580
 A:Note: conformation and properties are reported for a synthetic peptide corresponding to
 R:Label: S.; Gautel, M.; Lakey, A.; Trinick, J.
 EMBO J. 11, 1711-1716, 1992
 A:Title: Towards a molecular understanding of titin.
 A:Reference number: S20897; MUID:92258380; PMID:1582406
 A:Accession: S20898
 A:Status: nucleic acid sequence not shown
 A:Molecule type: mRNA
 A:Residues: 13597-14200, 'I', 14202-14596 <LAB2>
 A:Cross-references: EMBL:X64698; NID:g37192; PIDN:CAA45939.1; PID:g37193
 A:Accession: S20897
 A:Status: nucleic acid sequence not shown; translation not shown
 A:Molecule type: mRNA
 A:Residues: 16330-16382, 'S', 16384-16756, 'F', 16758-16860 <LAB3>
 A:Cross-references: EMBL:X64699; NID:g37190; PIDN:CAA45940.1; PID:g37191
 A:Accession: S20899
 A:Status: nucleic acid sequence not shown; translation not shown
 A:Molecule type: mRNA
 A:Residues: P', 22278-22431, 'R', 22433-22448, 'G', 22450-22453, 'Q', 22455-22480, 'TR', 22483-2
 A:Cross-references: EMBL:X64697; NID:g37190; PIDN:CAA45938.1; PID:g37195
 R:Kolmerer, B.; Olivieri, N.; Witt, C.C.; Hermand, B.G.; Labelt, S.
 J. Mol. Biol. 256, 556-563, 1996
 A:Title: Genomic organization of M line titin and its tissue-specific expression in two
 A:Reference number: S63665; MUID:96177761; PMID:8604138
 A:Accession: S63665
 A:Status: nucleic acid sequence not shown
 A:Molecule type: DNA
 A:Residues: 26729-26825 <COL>
 A:Cross-references: EMBL:X92412; NID:g1236761
 R:Gautel, M.; Leonard, K.; Labelt, S.
 EMBO J. 12, 3827-3834, 1993
 A:Title: Phosphorylation of KSP motifs in the C-terminal region of titin in differentia
 A:Reference number: S37393; MUID:94008990; PMID:8404852
 A:Accession: S37393
 A:Molecule type: mRNA
 A:Residues: 26831-26926 <GAU>
 R:Improta, S.; Pollou, A.S.; Pastore, A.
 submitted to the Brookhaven Protein Data Bank, February 1996

A:Reference number: A66736; PDB:1TIT
 A:Contents: annotation; conformation by (1)H-NMR, residues 5253-5341
 R:Frutli, H.; Pastore, A.
 submitted to the Brookhaven Protein Data Bank, August 1996
 A:Reference number: A66201; PDB:1NCT
 A:Contents: annotation; conformation by (1)H-NMR, residues 'S', 26059-26155
 C:Genetics:
 A:Gene: GDB:TTN
 A:Cross-references: GDB:127867; OMIM:188840
 A:Map position: 2q31-2q32
 C:Function:
 A:Description: structural protein forming filaments in striated muscle
 C:Superfamily: titin; fibronectin type III repeat homology; immunoglobulin homology;
 C:Keywords: alternative splicing; calmodulin binding; cardiac muscle; duplication; 91
 Structural protein
 F:24752-25008/Domain: protein kinase homology <KIN>
 F:184177-905, 2276, 2378, 2459, 2481, 2563, 2669, 2763, 2896, 3088, 3179, 3384, 3432, 3628, 3772, 40
 98, 11066, 11488, 11515, 11635, 11949, 12170, 12478, 12526, 12645, 12875, 13001, 13036, 13295, 1354
 tatus predicted
 F:16780, 16976, 17579, 17602, 17667, 17681, 17845, 17899, 18121, 18188, 18209, 18336, 18670, 18680
 , 21900, 21935, 22295, 22495, 22627, 22897, 23024, 23318, 23883, 24012, 24177, 24290, 24447, 24642,
 F:26171, 26178, 26184, 26190/Binding site: phosphate (Ser) (covalent) #status experiment

Query Match 11.68; Score 801.5; DB 1; Length 26926;
 Best Local Similarity 20.48; Pred. No. 9.8e-30;
 Matches 332; Conservative 204; Mismatches 489; Indels 599; Gaps 41;

QY 198 SPSLSERRSSVPIPIPADTRDNEVNHAEQOEAKRREAEQAASEAGDTPGSSPS 257
 Db 57 SPSD-----GRAKLTPAVTKANSGRYSL-----KATNSGQATSTAE 94
 QY 258 SLYSEPLGQPRFTQKLRSREVPEGRVOLDICVIGIPPOVRYTCGKLENSPDTHI 317
 Db 95 LLVKAET--APPNEFQRLQSNVTQGGSOVLRVYVGINPVVYKFDGAEIOSSLDQI 152
 QY 318 VQAGNLHSLITAEFEEDTGYSFCFASNIYGTSTSAEYIEG-----VSSDSGSD 369
 Db 153 SQEGDLSLLIAEAPDSGYGVYNATNSVGRATSEALLVQGEVEVPAAKTKTIVSTAQ 212
 QY 370 PNKEMNRIQK-----PNEVSSPPTTSVAVIPVAVP 399
 Db 213 ISESRQTRIEKKIEAHFEDARSIAVTVMIDGAAGQQLPHKTPRIPPKRSRPTPSIA 272
 QY 400 QAHLVAPRVATIQCCOSPTNYLQGLDGKPI-----IAAPVFTKMLQN 443
 Db 273 AKQAQLARQOSPSPRHSPSPVRHVRAPTSPVRSVSPAARISTPISRSVSELLARKTQA 332
 QY 444 -----LSASEGQL-----VVECEKVKCA- 461
 Db 333 SIVATGPEVPPPKQEGVVASSESAEARETTTLTSTQIRTEENWEGRYGVQEVVISGA 392
 QY 462 -----PSP 464
 Db 513 IKETEKFVPKVVISAAKAEQTRISEITKKQVQTEALMKETRTKTVVVKVIVATP 572
 QY 465 KVENY-----REGTLIEDSPDFRILQKKPRMAEPEEICTLVIAEVFAEDSGCTCT-- 516
 Db 573 KYKQDOLVSRGREG-ITTKRQVQITQEKAKKEAKETALSTIAVATAKAKEQETILRTRE 631
 QY 517 -----ASNKGYGVSSIAQLHVRGNEDLSNNGSLHSANST----- 550
 Db 632 TNATRQEQIOTVTHGKVDVGKAEAVATVVAADQARVREPRLHEESYAQQTILEGY 691
 QY 551 ---TNLAATEPOPSPHSEPSVQPPKPL----- 578

Db 692 KERISAAKVAEPPORPASEPHVYKAVPRVIAQPSETHIKTTDKGNHSSQIKKTTDL 751
 QY 579 --EGVLNHNHPRSSRISGLRVHF-----NLPEDDKGSEASSEAGVVTTRQ----- 622
 Db 752 TTERLVHVDKRPRTAS-----PHFTVSKISVPKTEHGYEASIAQSAIATLQKLSATSSA 806
 QY 623 -----TRPDSKORFENGQATKTPESFVKPEPPVLAKP-----KLDS 860
 Db 807 OKIKSVKATVPSETRV-----AEPTLPQFPADPTDYTKSEAGVKKVGVISFG 862
 QY 661 TOLQOLNOLV--LEOHOLNOLVPPSPKPEFFPMVNLNSNAPPATVTSXKOVKAPSSQTF 718
 Db 863 TVVREERFVHLGKREAKVTETARVAPVEIPV-----TPPTLVSLGNVTVIEGESV 914
 QY 719 SLARPKFFFTSTNT----- 733
 Db 915 TLECHISGYSPVTWYREDYQIESSIDFQISGIARLMIREAFEDSGRSTCSAVNE 974
 QY 734 AATVAPSS-----SPVFTLSSTPOTIQTYSKESLLVSHPSVOTKSPGGLSTQNEPLPP 787
 Db 975 ACTVSTCYLAVOVSEEFKETTAVTEKFTTEKRFVESRDVMTDT-----SLTEE--QA 1028
 QY 788 CPTETPTPPP-----TFISPGNOFQPRCV---SPIVPSPTSR----- 822
 Db 1029 GPGEPAAPIFTRKVPVOKLVGGGVYFCQVGNPKPRHYVKKSGVPLTGYRYKVSYNK 1088
 QY 823 -----IONVAFSLSSVLPSPALPPTNAMXLPSPASMPGOG 859
 Db 1089 QTGCKLVISMTFADGAGETIVVRNKHGCTSA---SASLLEADYELLAKSOEMLXQ- 1144
 QY 860 LAKNKTSPQVNDNIRET-----KNVIR-DLGKKTSDVRPNQOY 903
 Db 1145 -----TOTVAFVQEPVGTAGCFVSYEYKEQALIRKNAKTVVVRYVEDQEF 1199
 QY 904 KISSEORLANNEIEFLRTP-----VDESDDIOHDEIPTKCIAPIFDKRLKHFRTGEG 959
 Db 1200 HISSFERLKEIEYRIKTLLELLEDEGEEKMAVDISEASEVSGFDLRINKYRILEG 1259
 QY 960 SPVFTCKIVGIPVYVWFKDGKQISKRNECHKRRREGQCTSLHIESITSDDDNYTI 1019
 Db 1260 MGVTFCMKSGYPLPKIANYKDGKRI-KHGERYQNDFLQDGRASLRIPVLPDEGIYTA 1318
 QY 1020 MAANPOGRICRISGLMVGQ-----SL-----PIR----- 1042
 Db 1319 FASIKGNAICSGKLYVEAPALGAPTIIPILEPVSRISLSPRSVRSRPIRSPARMSP 1378
 QY 1043 SRLTSACQSHGRS-----RVQERDKLEPQERFRPHFTLOAPGDMVYAHGRLCDCKVSL 1099
 Db 1379 ARMSPARMSPARMSPGRRLEETDESOL-ERYLKPVFLKPVSEKLEGANCRCFDLKVGR 1437
 QY 1100 PPELTWLLNGQVLPDPASHRLMVRGTGVHSLLDPLTDQDAGTYKCIATNKTGQNSFSL 1159
 Db 1438 PMPETFWHDGQOIVNDYTHKVIKEDTQSLIIVPATPSDSGEMTVVAGNRAGRSSISV 1497
 QY 1160 ELSVVAKEVKAPVILEKQNGVPEGHPVLECRVIGMPPVYFKKKNETI-PCTRR 1218
 Db 1498 ILTVEAVEHVKPMFVEKLNKYNIEGSRLECKMVRATGNPNPDVLKNSDIIVPHKYPK 1557
 QY 1219 ISKHODTGTACLLIOPAKSDAGWYLTUSAKNEAGVSCVARTLOIYAQHHQIIPPMYSVR 1278
 Db 1558 IRI-EGTKGEAALKIDSTVSODSANYTATAINKAGROTTCKVNVVEFAEPEPERKLII 1616
 QY 1279 PGS 1282
 Db 1617 PRGT 1620

RESULT 4

T29757

Protein UNC-89 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 03-Dec-1999

C:Accession: T29757

R:Du, Z.; Le, T.T.; Wilson, R.
 submitted to the EMBL Data Library, May 1997
 A:Description: The sequence of C. elegans cosmid C09D1.
 A:Reference number: 220679
 A:Accession: T29757
 A:Status: Preliminary; translated from GB/EMBL/DDBJ
 A:Molecule type: DNA
 A:Residues: 16642 <DU2>
 A:Cross-references: EMBL:AF003131; PIDN:AAB54132.1; GSPDB:GN00019; CESP:unc-89
 A:Experimental source: strain Bristol N2; clone C09D1
 C:Genetics:
 A:Gene: CESP:unc-89
 A:Map position: 1
 A:Introns: 17/2; 108/3; 154/2; 211/2; 265/3; 326/2; 352/3; 426/2; 454/1; 500/1; 537/1
 /3; 5917/1; 6027/1; 6061/3; 6153/2; 6515/1; 6552/3; 6609/1

Query Match 8.88; Score 608; DB 2; Length 6642;
 Best Local Similarity 23.18; Pred. No. 4.3e-21;
 Matches 265; Conservative 160; Mismatches 468; Indels 252; Gaps 39;

QY 264 PLQPPRFTQKLSREVPEGARVQVDCIVVGIPIPPVQVRYWYCEGKELENS----- 312
 Db 2749 PRCEPPDFLEMLSNVRARTGTAKVHKVVTGDPKPSLTWYNNKELNSDLTYIVTDOKT 2808
 QY 313 -----PDHIVQAGNLHSLTAEAFEDTGRYSCFASNIYGTDSIAEIVIEG--- 360
 Db 2809 STLTINSFNPVHVGE-----IICKR-ENDAGEVSCITANMITYTSDMFSESEAEAE 2860
 QY 361 ---VSSSDSGDDPKKEMNR-----TOKPNEVSSPTTSATVPPVPAQO--- 402
 Db 2861 EFVGDDLTDESLREEMHRTPTVYMAPKFTIKDKTKAKKGSVAFECVVPDTKGVCKWK 2920
 QY 403 -----HLVAQPRVAT-----IQO-----CQSPTN 421
 Db 2921 LKDGKEIELIARVQRTGTGEGHITQELVDNVTEDACKYTCIVENTAGKDTCEATLT 2980
 QY 422 YLQGLDGKPLIAAPVTKMLONLSASGOLVVFECRVKAGSPKPKVMEYEGTLIEDSPDF 481
 Db 2981 VIESLEKKSEKKAPEFIVALKDKTKTKSEKVLCKVCEPRPKVSWLHDNVSRKKNNS 3040
 QY 482 -RLQKKPRMAPEEICTLVIAEVAEDSGCCTCTASNKTKTIVSSIAQLHVRG----- 534
 Db 3041 EXTITQESITVESVEGVERVTTITSELSHOCKYTCIAENTEGSKTEAFLTQGGAPVFT 3100
 QY 535 ---NEDLSNNSLHSANSTTNLAAIEPQPPSPHSPSPSVQEPAPKLEGVLVNHNEPRS 590
 Db 3101 KELQNKELSIGEKLVLSVKG---SPQ---PHVDYSPSETTKVE-----TKITS 3145
 QY 591 SSRIGLRVHFNLPEDDKGSEASSEAGVVTTRQTRPD-----SXOERFNCQATKTPESFP 645
 Db 3146 SSRIAI-----EHD---QNTNHRVVISQITKEDIVSKATNSIGTASTSKITTK 3195
 QY 646 VKEPPVLAKPKLDSTOLOQLHNOVLLEQHLQLOLPPPPSPKPEFPKMTVLNSNAPAVTT 705
 Db 3196 VCAP---VFEQGLKTSYKE-----KEEKMEKVVGGSGAPDVEN---FKDDKPVSEDG 3242
 QY 706 SXKOVKAPSSQTFSLARPKYFPFTNTTAATVAPSSPVFTLSST-----POTIQTQYTK 760
 Db 3243 NHMKKNPETGVFTLVWVKQ---AATDAGKYTAKASNPACTAESAEVTSLEKPTFV 3299
 QY 761 ESSLVSHPSVQTKSPGGLSIGNED-----LPQPTETPTPPPTFESIPSGNQFQPCVSP 818
 Db 3300 RELVITEVKINETATLSVTVKGVDPSPVEMKDGQPVQDSSHVIAKVEGSGSYITND 3359
 QY 815 IPVSTPS-----RIONPVAFIS-----SVLPSLPAIPTTNAMXL-PRSAFSPMSQGLAKKN 864
 Db 3360 ARLEDGSGYACRATNPAGEAKTEANFAVXNL--VPEFVEKLVSLPEVKEKESTTSLVKV 3417
 QY 865 TKSPQ-----PVNDDNIR---ETKNVIRDLGK-KITESDVRPNQOQYKISSFQR 911
 Db 3418 VGTPEPSVEMFKDDTPISIDNVHVIQQTAV---GSFSLTINDARQGD---VGIYSR 3469
 QY 912 LANEIEFLRTPVDESDEIQHDEIPTKCIAPIFDKRLKHFRTGEGSPVFTTCTKIVGI 971